

- a) transforming a seed-bearing plant, or a progenitor of the seed-bearing plant, with a vector comprising the nucleic acid of claim 1;
  - b) growing the seed-bearing plant to obtain seed under conditions wherein the nucleic acid sequence is expressed during embryogenesis under the control of the transcriptional regulatory region to alter the phenotype of the seed.
20. (amended) A method of transforming a plant cell comprising transforming the plant cell with the recombinant nucleic acid of claim 1.

### REMARKS

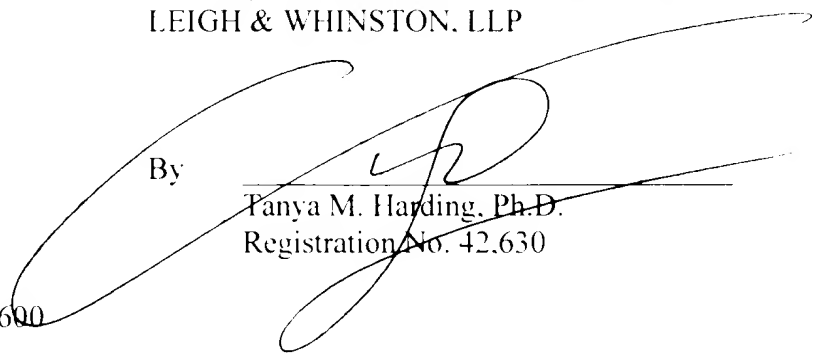
By this preliminary amendment, the specification is amended to add the priority claim to related cases. Claims 7, 12, 14, 15, 16, 19, and 20 are amended to remove multiple dependencies, and claims 2, 3, 4, 5, 8, 9, 10, and 11 are amended to provide reference to the SEQ ID NO for the indicated sequences.

No new matter has been added by this amendment. Nor was this amendment made for any purpose related to statutory requirements of patentability; rather, the changes are related to purely economic considerations and are in no way meant to limit the scope of any claim.

Respectfully submitted,

KLARQUIST SPARKMAN CAMPBELL  
LEIGH & WHINSTON, LLP

By

  
Tanya M. Harding, Ph.D.  
Registration No. 42,630

One World Trade Center, Suite 1600  
121 S.W. Salmon Street  
Portland, Oregon 97204  
Telephone: (503) 226-7391  
Facsimile: (503) 228-9446

**Marked-up Version of the Claims  
Pursuant to 37 C.F.R. §§ 1.121(b)-(c)**

1. A recombinant nucleic acid molecule comprising a heterologous promoter sequence operably linked to a nucleic acid sequence, wherein the promoter sequence comprises a transcriptional regulatory region capable of mediating seed-specific expression in *Arabidopsis* wherein the transcriptional regulatory region:
  - (a) is obtainable from a 5' region of a plant *FAEI* gene; or
  - (b) hybridizes under stringent conditions to the 5' region of the plant *FAEI* gene; or
  - (c) is at least 70% identical when optimally aligned to the 5' region of the plant *FAEI* gene.

2. (amended) The recombinant nucleic acid of claim 1 wherein the 5' region of the plant *FAEI* gene comprises (5' to 3'):

AGA TCTAAGAACA CACATTCCCT CAAATTTTAA TGCACATGTA ATCATAAGTTT  
AGCACAATTC AAAAATAATG TAGTATTAAA GACAGAAATT TGTAGACTTT TTTTGGCGT  
TAAAGGAAGA CTAASTTTAT AGGTACATTT TATTTTAAST GGAAAAACGA AATTTTCCAT  
CGAAATATAT GAATTTAGTA TATATAATTC TGCAATGTA C TATTTTGCTA TTTTGGCAAC  
TTTCAGTGGA CTACTACTTT ATTACAATGT GTATGGATGC ATGAGTTTGA GTATACACAT  
GTCTAAATGC ATGCTTTGCA AAACGTAACG GACCACAAAA GAGGATCCAT GCAAATACAT  
CTCATAGCTT CCTCCATTAT TTTCCGACAC AAACAGAGCA (SEQ ID NO: 15).

3. (amended) The recombinant nucleic acid of claim 1 wherein the 5' region of the plant *FAEI* gene comprises (5' to 3'):

AAGGCTTACC CTATTAGTTG AAAGTTGAAA CTTTGTTCCT TACTCAATTC CTAGTTGTGT  
AAATGTATGT ATATGTAATG CGTATAAAAC GTAGTACTTA AATGACTAGG AGTGGTTCTT  
GAGACCGATG AGAGATGGGA GCAGAACTAA AGATGATGAC ATAATTAAGA AGGAATTTGA  
AAGGCTCITA GGTTTGAATC CTATTCGAGA ATGTTTTTGT CAAAGATAGT GGCGATTTTG  
AACCAAAGAA AACATTTAAA AAATCAGTAT CCGGTTACGT TCATGCCAAT AGAAAGTGGT  
CTAGGATCTG ATTGTAATTT TAGACTTAAA GAGTCTCTTA AGATTCAATC CTGGCTGTGT  
ACAAAACCTAC AAATAATATA TTTTAGACTA TTTGGCCTTA ACTAACTTC CACTCATTAT  
TTACTGAGGT TAGAGAATAG ACTTGCGAAT AAACACATTC CCGAGAAATA CTCATGATCC

CATAATTAGT CAGAGGGTAT GCCAATCAGA TCTAAGAAACA CACATTCCCT CAAATTTTAA  
TGCACATGTA ATCATASTTT AGCACAATTG AAAAATAATG TAGTATTAAA GACAGAAATT  
TGTAGACTTT TTTTGGGCT TAAAGGAAGA CTAAGTTTAT AGGTACATTT TATTTTAAST  
GGAAAACCGA AATTTTCCAT CGAAATATAT GAATTTAGTA TATATATTTG TGCAATGTAC  
TATTTTGCTA TTTTGGCAAC TTTCAGTGGG CTACTACTTT ATTACAATGT STATGGATGC  
ATGAGTTTGA GTATACACAT GTCTAAATGC ATGCTTTTGA AAACGTAACG GACCACAAAA  
GAGGATCCAT GCAAATACAT CTCATAGCTT COTCCATTAT TTTCCGACAC AAACAGAGCA  
(SEQ ID NO: 16).

4. (amended) The recombinant nucleic acid of claim 1 wherein the 5' region of the plant  
*FAE1* gene comprises (5' to 3'):

CTGACTTC ACCAAAGAAA CAACTCGAGT CGTTATCCAT CTCTCATAA  
CCATCGCTCC ACTCTTTGCC TTCACGGTTT TCGGTTGGGT TCTCTACATC GCAACCCGGC  
CCAAACCGGT TTACCTCGTT GAGTACTCAT GTACCTTCC ACCAACGCAT TGTAGATCAA  
GTATCTCCAA GGTCATGGAT ATCTTTTATC AAGTAAGAAA AGCTGATCCT TCTCGGAACG  
GCACGTGCGA TGACTCGTCC TGGCTTGACT TCTTGAGGAA GATTCAAGAA CGTTCAGSTC  
TAGGGGATGA AACTCAGGGG CCGGAGGGGC TGCTTCAGST CCGTCCCGGG AAGACTTTTG  
CGGCGGCGCG TGAAAGAGACG GAGCAAGTTA TCATTGGTGC GCTAGAAAAT CTATTCAGAA  
ACACCAACGT TAACCTCTAA GATATAGGTA TACTTGTGCT GAACTCAAGC ATGTTTAATC  
CAACTCCATC GCTCTCCGCG ATGGTGGTTA ACACTTTCAA GCTCCGAAGC AACGTAAGAA  
GCTTTAACCT TGGTGGCATG GGTGTAGTG CCGGCGTTAT AGCCATTGAT CTAGCAAAGG  
ACTTGTTCGA TGTCATATAA AATACGTATG CTCTTGTGCT GAGCACAGAG AACATCACTT  
ATAACATTTA CGCTGCTGAT AATAGGTCCA TGATGCTTTC AAATTGCTTG TCCGCTGTTG  
GTGGGGCCCG TATTTTGCTC TCCAAACAAGC CTGGAGATCG TAGACGGTCC AAGTACGAGC  
TAGTTCACAC GGTTCGAACG CATACGGGAG CTGACGACAA GTCTTTTCGT TGCGTGCAAC  
AAGGAGACGA TGAGAACGGC AAAATCGGAG TGAGTTTGTC CAAGGACATA ACCGATGTTG  
CTGGTCCGAAC GGTAAAGAAA AACATAGCAA CGTTGGGTCC GTTGATTCTT CCGTTAAGCG  
AGAACTTCT TTTTTTGGTT ACCTTCATGG GCAAGAAACT TTTCAAAGAT AAAATCAAAC  
ATTACTACGT CCGGGATTTG AAAGTTGCTA TTGACCATTT TTGTATACAT GCGGGAGGCA  
GAGCGTGAT TGATGTGCTA GAGAAGAACC TAGCCCTAGC ACCGATCGAT GTAGAGGCAT  
CAAGATCAAC GTTACATAGA TTTGSAACA CTTCATCTAG CTCAATATGG TATGAGTTGG  
CATACATAGA AGCAAAAGGA AGGATGAAGA AAGTAATAA AGTTTGGCAG ATTGCTTTAG  
GGTCAGGCTT TAAGTGTAAAG AGTGCASTTT GGGTGGCTCT AAACAATGTC AAAGCTTCGA  
CAAAATAGTCC TTGGGAACAC TGCATCGACA GATACCGGGT CAAAATTGAT TCTGATTGAG

GTAAAGTACAG GACTCGTGT CAAAACGGTC GGTCCTAATA AACGATGTTT GCTCTCTTTC  
TTTTCTTTTT ATTTGTTATA ATAATTTGAT GGCTACGATG TTTCTCTTGT TTGTTATGAA  
TAAAGAATGC AATGGTGTTC TAGTATTTGA TTGTTTTACA TGTATGTATC TCTTATTTAC  
ATGAAATTTT TAAACGCCTA AAAAAAAAAA CGGAATTCCG (SEQ ID NO: 17).

5. (amended) The recombinant nucleic acid of claim 1 wherein the 5' region of the plant  
*FAEI* gene comprises (5' to 3'):

CAGCTTAAC CGGTAAAATT GGCTGTACA  
TATATTTACC ACTGAGTAAA GACATCAGTT AATGATTTGT TGTTACTCAA TTGGGCTAAG  
TGTATTATTA TATGTGTTGT ATATAATAAA GGTAGAACGT AAATTIAC TA AGAATGTGTT  
TTTCCAATGT GATTGCTCTT TGGGCTCTTA GGTTTGAATC CTACTCGAGA AACTAATTT  
TAATTTACTG GCAAAAATAG AAATCAATTT ATAAGTGTTC AAACAAATCG ATGGTATAAC  
TGATTAGTGA TCACTCTTAG GTTTTGATCC AACTCGAGTA TTGAGTATTG AACGCTTTTT  
TTAAATAAAA TCTTGATTTT TAAATTGGTT TTTTGAGTAA AAAAGTTCTT AATATTTTCT  
CTTTGTTTTA ATGGGTTTGT TTTGCATTTT ATAAGCTTAA TTTTCTAAT TTAATATTTT  
ATCTATCATC GTCGTAAGG TTTTATTGG CACAACTTG TTTTACTTTT CTACCTTATA  
ATTTGGGAAC TGTTGAGTC AAAGCGTACC GGACAAATAT GTTTTATATT CTTATTTAAG  
AATTAACTACT CATCTATAA TTAGTCAGAG GCTAGGGAGA TTCAGCCAAT CAATGCTAAC  
AACAAAATTC TCTTAATGAT CTAACGATGC TATTTAATAT TCGGATCAGT ATTCTTAAAT  
AAGAATATAA AACTAATTCA ATAGTTACAG ATAAAACTT ATATAGACTT TTTTATTTGG  
AATATAAAG TATCAATATA TTATAGACAA TATTTATAAC GTTAAAAATA CAATATTTAT  
ATTTTTTATA TATTTATTTT AAATTGAAAA GCATTACTTC TATCGAAATG AATTTTAGTA  
TATTAATTAA TATTTTTTTA ATCGGACTAC TTTCTATTTT TGGCAGCTTT CATCTGACTA  
CTAATTTATT TCAATGTGTA TGCATGCATG AGCATGAGTA ATACACATGT CTATATAAAT  
GCATGTAAAA CGTAACGGAC CACAAAAGTG GATCCATACA AATACATCTC ATCGCACCTT  
CTCCGACACA AAAGTGAACA\_ (SEQ ID NO: 18).

6. The recombinant nucleic acid of claim 1 wherein the promoter sequence is selected from  
the group consisting of *Arabidopsis thaliana*, *Lunaria annua* and *Brassica napus FAEI*  
promoter sequences.

7. (amended) The recombinant nucleic acid of ~~any one of claims 1 through 6~~ claim 6, wherein the transcriptional regulatory region is at least 70% identical when optimally aligned to the 5' region of the plant *FAE1* gene.

8. (amended) The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):

AGA TCTAAGAAC CACATTCCCT CAAATTTTAA TGCACATGTA  
ATCATAGTTT AGCACAATTC AAAAATAATG TAGTATTAAA GACAGAAATT TGTAGACTTT  
TTTTTGGCGT TAAAGGAAGA CTAAGTTTAT ACGTACATTT TATTTTAAAGT GGAAAAACGA  
AATTTTCCAT CGAAATATAT GAATTTAGTA TATATATTTT TGCATGTAC TATTTTGGTA  
TTTTGGCAAC TTTCAGTGGC CTACTACTTT ATTACAATGT GTATGGATGC ATGAGTTTGA  
GTATACACAT GTCTAAATGC ATGCTTTGCA AAACGTAACG GACCACAAAA GAGGATCCAT  
GCAAATACAT CTCATAGCTT CCTCCATTAT TTTCGGACAC AAACAGAGCA (SEQ ID  
NO: 15).

9. (amended) The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):

AAGGCTTACC CTATTAGTTG AAAGTTGAAA CTTTGTTCCT TACTCAATTC CTAGTTGTGT  
AAATGTATGT ATATGTAATG CGTATAAAAC GTAGTACTTA AATGACTAGG AGTGGTTCTT  
GAGACCGATG AGAGATGGGA GCAGAACTAA AGATGATGAC ATAATTAAAG ACGAATTTGA  
AAGGCTCTTA GGTTTGAATC CTATTGAGA ATGTTTTTTGT CAAAGATAGT GCGGATTTTG  
AACCAAAAGAA AACATTTAAA AAATCAGTAT CCGGTTACGT TCATGCAAT AGAAAGTGGT  
CTAGGATCTG ATTGTAATTT TAGACTTAAA GAGTCTCTTA AGATTCATTC CTGGCTGTGT  
ACAAAACAC AAATAATATA TTTTAGACTA TTTGGGCTTA ACTAACTTC CACTCATTAT  
TTACTGAGGT TAGAGAATAG ACTTGGGAAT AAACACATTC CCGAGAAATA CTCATGATCC  
CATAATTAGT CAGAGGGTAT GCGAATCAGA TCTAAGAAC CACATTCCCT CAAATTTTAA  
TGCACATGTA ATCATAGTTT AGCACAATTC AAAAATAATG TAGTATTAAA GACAGAAATT  
TGTAGACTTT TTTTTGGCGT TAAAGGAAGA CTAAGTTTAT ACGTACATTT TATTTTAAAGT  
GGAAAAACGA AATTTTCCAT CGAAATATAT GAATTTAGTA TATATATTTT TGCATGTAC  
TATTTTGGTA TTTTGGCAAC TTTCAGTGGC CTACTACTTT ATTACAATGT GTATGGATGC  
ATGAGTTTGA GTATACACAT GTCTAAATGC ATGCTTTGCA AAACGTAACG GACCACAAAA  
GAGGATCCAT GCAAATACAT CTCATAGCTT CCTCCATTAT TTTCGGACAC AAACAGAGCA  
(SEQ ID NO: 16).

10. (amended) The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):

CTGACTTC ACCAAAGAAA CAACTCGAGT CGTTATCCAT CTGCTCATAA  
CCATCGCTCC ACTCTTTGCC TTCACCGTTT TCGGTTCCGT TCTCTACATC GCAACCCGGC  
CCAAACCCGT TTACCTCGTT GAGTACTCAT GCTACCTTCC ACCAACGCAT TGTAGATCAA  
GTATCTCCAA GGTGATGGAT ATCTTTTATC AAGTAAGAAA AGCTGATCCT TCTCGGAACG  
GCACGTGCGA TGACTCGTCC TGGCTTGAAT TCTTGAGGAA GATTCAAGAA CGTTCAGGTC  
TAGGCGATGA AACTCAGGGG CCGGAGGGGC TGCTTCAGGT CCTCCCGGG AAGACTTTTG  
CGGCGGCGCG TGAAGAGACG GAGCAAGTTA TCATTGGTGC GCTAGAAAAT CTATTCAAGA  
ACACCAACGT TAACCTTAAA GATATAGGTA TACTTGTGGT GAACTCAAGC ATGTTTAATC  
CAACTCCATC GCTCTCCGCG ATGGTGGTTA ACACCTTCAA GCTCCGAAGC AAGTAAGAA  
GCTTTAACCT TGGTGGCATG GGTGTAAGTG CCGGCGTTAT AGCCATTGAT CTAGCAAAAG  
ACTTGTTGCA TGTCATATAA AATACGTATG CTCTTGTGCT GAGCACAGAG AACATCACTT  
ATAACATTTA CGCTGGTGAT AATAGGTCCA TGATGGTTTC AAATTGCTTG TTCGGTGTG  
GTGGGGCCGC TATTTTGCTC TCCAACAAGC CTGGAGATCG TAGACGGTCC AAGTACGAGC  
TAGTTCACAC GGTTCGAACG CATACCGGAG CTGACGACAA GTCTTTTCTG TGGTGCAAC  
AAGGAGACGA TGAGAACGGC AAAATCGGAG TGAGTTTGTG CAAGGACATA ACCGATGTTG  
CTGCTCGAAC GGTAAAGAAA AACATAGCAA CGTTGGGTCC GTTGATTCTT CCGTTAAGCG  
AGAAACTTCT TTTTTTGGTT ACCTTCATGG GCAAGAAACT TTTCAAAGAT AAAATCAAAC  
ATTACTACGT CCGGATTTTC AAACTTGGTA TTGACCATTT TTGTATACAT GCGGAGGGCA  
GAGCGGTGAT TGATGTGCTA GAGAAGAACG TAGCCCTAGC ACCGATCGAT GTAGAGGCAT  
CAAGATCAAC GTTACATAGA TTTGGAAACA CTTCATCTAG CTCAATATGG TATGAGTTGG  
CATACATAGA AGCAAAAAGA AGGATGAAGA AAGGTAATAA AGTTTGGCAG ATTGCTTTAG  
GGTCAGGCTT TAAGTGTAAC AGTGCACTTT GGCTGGCTCT AAACAATGTC AAAGCTTCGA  
CAAAATAGTCC TTGGGAACAC TGCATCGACA GATACCCGGT CAAAATTGAT TCTGATTCCG  
GTAAAGTCAG GACTCGTGTG CAAAACGGTC GGTCTAATA AACGATGTTT GCTCTCTTTC  
GTTTCTTTTT ATTTGTTATA ATAATTTGAT GGCTACGATG TTTCTCTTGT TTGTTATGAA  
TAAAGAATGC AATGGTGTTC TAGTATTTGA TTGTTTTACA TGTATGTATC TCTTATTTAC  
ATGAAATTTT TAAACGGCTA AAAAAAAAAA CGGAATTCGG (SEQ ID NO: 17).

11. (amended) The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):

CAGCTTAAC CGGTAAAATT GGCTGTACA  
TATATTTACC ACTGASTAAA GACATCAGTT AATGATTTGT TGTACTCAA TTGGGCTAAG  
TGTATTATTA TATGTGTTGT ATATAATAAA GGTAGAACGT AAATTTACTA AGAATGTGTT  
TTTCCAATGT GATTGCTCTT TGGCCTCTTA GGTTCGAATC CTACTCGAGA AGACTAATTT  
TAATTTACTG GCAAAAATAG AAATCAATTT ATAAGTGTTC AAACAAATCG ATGGTATAAC  
TGATTAGTGA TCACTCTTAG GTTTTGATCC AACTCGAGTA TTGAGTATTG AACGCTTTTT  
TTAAATAAAA TCTTGATTTT TAAATTGGTT TTTTGASTAA AAAAGTTCTT AATATTTTCT  
CTTTGTTTTA ATGGGTTTGT TTTGCATTTT ATAAGCTTAA TTTTCTAAT TTAATATTTT  
ATCTATCATE GTCGGTAAAG TTTTATTTGG CACAAACTTG TTTTACTTTT CTACCTTATA  
ATTTGGGAAC TGGTTGAGTC AAAGCGTACC GGACAAATAT GTTTTATATT CTTATTTAAG  
AATTAACACT CATCTATAA TTAGTCAGAG GCTAGGAGAG TTCAGCCAAT CAATGCTAAC  
AACAAAATTC TCTTAATGAT CTAACGATGC TATTTAATAT TCGGATCAGT ATTCTTAAAT  
AAGAATATAA AACTAATTCA ATAGTTACAG ATAAAACTT ATATAGACTT TTTTATTTGG  
AATATAAAAG TATCAATATA TTATAGACAA TATTTATAAC GTTAAAAATA CAATATTTAT  
ATTTTTTATA TATTTATTTT AAATTGAAAA GCATTACTTC TATCGAAATG AATTTTAGTA  
TATTAATTAA TATTTTTTTA ATCGGACTAC TTCTCTATTT TGGCACCTTT CATCTGACTA  
CTAATTTATT TCAATGTGTA TGCATGCATG AGCATGAGTA ATACACATGT CTATATAAAT  
GCATGTAAAA CGTAACGGAC CACAAAAGTG GATCCATACA AATACATCTC ATCGCACCCCT  
CTCCGACACA AAAGTGAACA (SEQ ID NO: 18).

12. (amended) The recombinant nucleic acid of ~~any of claims 1 through 11~~ claim 1 wherein the nucleic acid sequence encodes a translatable mRNA.
13. The recombinant nucleic acid of claim 12 wherein the nucleic acid sequence encodes an enzyme involved in lipid metabolism.
14. (amended) The recombinant nucleic acid of ~~any one of claims 1 through 13~~ claim 13, further comprising a transcription termination region operably linked to the nucleic acid sequence.
15. (amended) A host cell comprising the recombinant nucleic acid of ~~any one of claims 1 through 14~~ claim 14.

16. The host cell of claim 15, wherein the host cell is of a dicotyledonous plant species.
17. (amended) A plant comprising the recombinant nucleic acid of ~~any one of claims 1 through 14~~ claim 14.
18. The plant of claim 17, wherein the plant is of a dicotyledonous plant species.
19. (amended) A method of altering the phenotype of a seed comprising:
  - a) transforming a seed-bearing plant, or a progenitor of the seed-bearing plant, with a vector comprising the nucleic acid of ~~any one of claims 1 through 14~~ claim 1;
  - b) growing the seed-bearing plant to obtain seed under conditions wherein the nucleic acid sequence is expressed during embryogenesis under the control of the transcriptional regulatory region to alter the phenotype of the seed.
20. (amended) A method of transforming a plant cell comprising transforming the plant cell with the recombinant nucleic acid of ~~any one of claims 1 through 14~~ claim 1.



11. (amended) The recombinant nucleic acid of claim 1 wherein the transcriptional regulatory region comprises (5' to 3'):

CAGCTTAAC CGGTAAAATT GGCTGTACA  
TATATTTACC ACTGAGTAAA GACATCASTT AATGATTTGT TGTTACTCAA TTGGGCTAAG  
TGTATTATTA TATGTGTTGT ATATAATAAA GSTAGAACGT AAATTTACTA AGAATGTGTT  
TTTCCAATGT GATTGCTCTT TGGCCTCTTA GGTTCGAATC CTACTCGAGA AGACTAATTT  
TAATTTACTG GCAAAAATAG AAATCAATTT ATAAGTGTTT AAACAAATCG ATGGTATAAC  
TGATTAGTGA TCACTCTTAG GTTTTGATCC AACTCGAGTA TTGAGTATTG AACGCTTTTT  
TTAAATAAAA TCTTGATTTT TAAATTGCTT TTTTGAGTAA AAAAGTTCTT AATATTTTCT  
CTTTGTTTTA ATGGGTTTGT TTTGCATTTT ATAAGCTTAA TTTTCTAAT TTAATATTTT  
ATCTATCATE GTCGTAAG TTTTATTTGG CACAACTTG TTTTACTTTT CTACCTTATA  
ATTTGGGAAC TGGTTGAGTC AAAGCGTACC GGACAAATAT GTTTTATATT CTTATTTAAG  
AATTAACACT CATCTCATAA TTAGTCAGAG GCTAGGGAGA TTCAGCCAAT CAATGCTAAC  
AACAAAATTC TCTTAATGAT CTAACGATGC TATTTAATAT TCGGATCAGT ATTCTTAAAT  
AAGAATATAA AACTAATTCA ATAGTTACAG ATAAAACTT ATATAGACTT TTTTATTTGG  
AATATAAAAG TATCAATATA TTATAGACAA TATTTATAAC GTTAAAAATA CAATATTTAT  
ATTTTTTATA TATTTATTTT AAATTGAAAA GCATTACTTC TATCGAAATG AATTTTAGTA  
TATTAATTAA TATTTTTTTT ATCGGACTAC TTCTTATTTT TGGCAGCTTT CATCTGACTA  
CTAATTTATT TCAATGTGTA TGCATGCATG AGCATGAGTA ATACACATGT CTATATAAAT  
GCATGTAAAA CGTAACGGAC CACAAAAGTG GATCCATACA AATACATCTC ATCGCACCCCT  
CTCCGACACA AACTGAACA (SEQ ID NO: 13).

12. (amended) The recombinant nucleic acid of claim 1 wherein the nucleic acid sequence encodes a translatable mRNA.
14. (amended) The recombinant nucleic acid of claim 13, further comprising a transcription termination region operably linked to the nucleic acid sequence.
15. (amended) A host cell comprising the recombinant nucleic acid of claim 14.
17. (amended) A plant comprising the recombinant nucleic acid of claim 14.
19. (amended) A method of altering the phenotype of a seed comprising: